

SEQUENCE LISTING

SEQ ID NO: 1 is a mouse 312C2 nucleic acid sequence.
SEQ ID NO: 2 is a mouse 312C2 amino acid sequence.
SEQ ID NO: 3 is a human 312C2 nucleic acid sequence.
SEQ ID NO: 4 is a human 312C2 amino acid sequence.
SEQ ID NO: 5 is a reverse translation sequence.
SEQ ID NO: 6 is clone A8 amino acid sequence.
SEQ ID NO: 7 is clone A5 amino acid sequence.
SEQ ID NO: 8 is clone G10 amino acid sequence.

(1) GENERAL INFORMATION:

(i) APPLICANT: Gorman, Daniel M.
Randall, Troy D.
Zlotnik, Albert

(ii) TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED REAGENTS

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/911,423
(B) FILING DATE: 14-AUG-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/023,419
(B) FILING DATE: 16-AUG-1996

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/027,901
(B) FILING DATE: 07-OCT-1996

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: DX0612K

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 68..751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

20	CTCGAGATCC ATTGTGCTGG AAAGGGAACCT CCTGAAATCA GCCGACAGAA GACTCAGGAG	60
	AAGCACT ATG GGG GCA TGG GCC ATG CTG TAT GGA GTC TCG ATG CTC TGT	109
	Met Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys	
	1 5 10	
25	GTG CTG GAC CTA GGT CAG CCG AGT GTA GTT GAG GAG CCT GGC TGT GGC	157
	Val Leu Asp Leu Gly Gln Pro Ser Val Val Glu Glu Pro Gly Cys Gly	
	15 20 25 30	
30	CCT GGC AAG GTT CAG AAC GGA AGT GGC AAC AAC ACT CGC TGC TGC AGC	205
	Pro Gly Lys Val Gln Asn Gly Ser Gly Asn Asn Thr Arg Cys Cys Ser	
	35 40 45	
35	CTG TAT GCT CCA GGC AAG GAG GAC TGT CCA AAA GAA AGG TGC ATA TGT	253
	Leu Tyr Ala Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys	
	50 55 60	
40	GTC ACA CCT GAG TAC CAC TGT GGA GAC CCT CAG TGC AAG ATC TGC AAG	301
	Val Thr Pro Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys	
	65 70 75	
45	CAC TAC CCC TGC CAA CCA GGC CAG AGG GTG GAG TCT CAA GGG GAT ATT	349
	His Tyr Pro Cys Gln Pro Gly Gln Arg Val Glu Ser Gln Gly Asp Ile	
	80 85 90	
50	GTG TTT GGC TTC CGG TGT GTT GCC TGT GCC ATG GGC ACC TTC TCC GCA	397
	Val Phe Gly Phe Arg Cys Val Ala Cys Ala Met Gly Thr Phe Ser Ala	
	95 100 105 110	
55	GGT CGT GAC GGT CAC TGC AGA CTT TGG ACC AAC TGT TCT CAG TTT GGA	445
	Gly Arg Asp Gly His Cys Arg Leu Trp Thr Asn Cys Ser Gln Phe Gly	
	115 120 125	
60	TTT CTC ACC ATG TTC CCT GGG AAC AAG ACC CAC AAT GCT GTG TGC ATC	493
	Phe Leu Thr Met Phe Pro Gly Asn Lys Thr His Asn Ala Val Cys Ile	
	130 135 140	

CCG GAG CCA CTG CCC ACT GAG CAA TAC GGC CAT TTG ACT GTC ATC TTC 541
Pro Glu Pro Leu Pro Thr Glu Gln Tyr Gly His Leu Thr Val Ile Phe
145 150 155

CTG GTC ATG GCT GCA TGC ATT TTC TTC CTA ACC ACA GTC CAG CTC GGC 589
Leu Val Met Ala Ala Cys Ile Phe Phe Leu Thr Thr Val Gln Leu Gly
160 165 170

CTG CAC ATA TGG CAG CTG AGG AGG CAA CAC ATG TGT CCC CGA GAG ACC 637
Leu His Ile Trp Gln Leu Arg Arg Gln His Met Cys Pro Arg Glu Thr
175 180 185 190

CAG CCA TTC GCG GAG GTG CAG TTG TCA GCT GAG GAT GCT TGC AGC TTC 685
Gln Pro Phe Ala Glu Val Gln Leu Ser Ala Glu Asp Ala Cys Ser Phe
195 200 205

CAG TTC CCT GAG GAG GAA CGC GGG GAG CAG ACA GAA GAA AAG TGT CAT 733
Gln Phe Pro Glu Glu Glu Arg Gly Glu Gln Thr Glu Glu Lys Cys His
210 215 220

CTG GGG GGT CGG TGG CCA TGAGGCCTGG TCTTCCTCTG TGCCCCAAGC 781
Leu Gly Gly Arg Trp Pro
225

CAGACGCTAC AAGACTTGCC CAGCTATAACC CTTGGTGAGA GCAGGGGCCA TGCTCTGCAC 841

CCTTCCCTGG GCCTGGCCCT GCTCCCCTCA ACAGTGGCGG AAGTGGGTGT ATGAGAGCGG 901

TGAGTTACGA TTGGGCCCTA TGGCTGCCTT TCTCATTGA CAGCTCTGTT GGAGTAGGGT 961

CTTTGGGCCC ACCAAGAGCA CCACGTTTAG CACAAGATCT TGTACAAGAA TAAATACTTG 1021

TTTAGTAACC TGAAAAAAAAA AAAAAAAGG GCGGCCGCGG AGGCCGAATT CC 1073

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys Val Leu
1 5 10 15

Asp Leu Gly Gln Pro Ser Val Val Glu Glu Pro Gly Cys Gly Pro Gly
20 25 30

Lys Val Gln Asn Gly Ser Gly Asn Asn Thr Arg Cys Cys Ser Leu Tyr
35 40 45

Ala Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys Val Thr
50 55 60

Pro Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys His Tyr
65 70 75 80

5 Pro Cys Gln Pro Gly Gln Arg Val Glu Ser Gln Gly Asp Ile Val Phe
85 90 95

Gly Phe Arg Cys Val Ala Cys Ala Met Gly Thr Phe Ser Ala Gly Arg
100 105 110

10 Asp Gly His Cys Arg Leu Trp Thr Asn Cys Ser Gln Phe Gly Phe Leu
115 120 125

15 Thr Met Phe Pro Gly Asn Lys Thr His Asn Ala Val Cys Ile Pro Glu
130 135 140

Pro Leu Pro Thr Glu Gln Tyr Gly His Leu Thr Val Ile Phe Leu Val
145 150 155 160

20 Met Ala Ala Cys Ile Phe Phe Leu Thr Thr Val Gln Leu Gly Leu His
165 170 175

Ile Trp Gln Leu Arg Arg Gln His Met Cys Pro Arg Glu Thr Gln Pro
180 185 190

25 Phe Ala Glu Val Gln Leu Ser Ala Glu Asp Ala Cys Ser Phe Gln Phe
195 200 205

30 Pro Glu Glu Glu Arg Gly Glu Gln Thr Glu Glu Lys Cys His Leu Gly
210 215 220

Gly Arg Trp Pro
225

35 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1006 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

45 (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..723

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG GCA CAG CAC GGG GCG ATG GGC GCG TTT CGG GCC CTG TGC GGC CTG
Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu

1

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10

15

48

	GCG CTG CTG TGC GCG CTC AGC CTG GGT CAG CGC CCC ACC GGG GGT CCC	96
	Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro	
	20 25 30	
5	GGG TGC GGC CCT GGG CGC CTC CTG CTT GGG ACG GGA ACG GAC GCG CGC	144
	Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg	
	35 40 45	
10	TGC TGC CGG GTT CAC ACG ACG CGC TGC TGC CGC GAT TAC CCG GGC GAG	192
	Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu	
	50 55 60	
15	GAG TGC TGT TCC GAG TGG GAC TGC ATG TGT GTC CAG CCT GAA TTC CAC	240
	Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His	
	65 70 75 80	
20	TGC GGA GAC CCT TGC TGC ACG ACC TGC CGG CAC CAC CCT TGT CCC CCA	288
	Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro	
	85 90 95	
25	GGC CAG GGG GTA CAG TCC CAG GGG AAA TTC AGT TTT GGC TTC CAG TGT	336
	Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys	
	100 105 110	
30	ATC GAC TGT GCC TCG GGG ACC TTC TCC GGG GGC CAC GAA GGC CAC TGC	384
	Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys	
	115 120 125	
35	AAA CCT TGG ACA GAC TGC ACC CAG TTC GGG TTT CTC ACT GTG TTC CCT	432
	Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro	
	130 135 140	
40	GGG AAC AAG ACC CAC AAC GCT GTG TGC GTC CCA GGG TCC CCG CCG GCA	480
	Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala	
	145 150 155 160	
45	GAG CCG CTT GGG TGG CTG ACC GTC GTC CTC CTG GCC GTG GCC GCC TGC	528
	Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys	
	165 170 175	
50	GTC CTC CTC CTG ACC TCG GCC CAG CTT GGA CTG CAC ATC TGG CAG CTG	576
	Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu	
	180 185 190	
55	AGG AGT CAG TGC ATG TGG CCC CGA GAG ACC CAG CTG CTG CTG GAG GTG	624
	Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Leu Glu Val	
	195 200 205	
60	CCG CCG TCG ACC GAA GAC GCC AGA AGC TGC CAG TTC CCC GAG GAA GAG	672
	Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu	
	210 215 220	
65	CGG GGC GAG CGA TCG GCA GAG GAG AAG GGG CGG CTG GGA GAC CTG TGG	720
	Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp	
	225 230 235 240	

GTG TGAGCCTGGC CGTCCTCCGG GGCCACCGAC CGCAGCCAGC CCCTCCCCAG 773
Val

5 GAGCTCCCCA GGCCGCAGGG GCTCTGCGTT CTGCTCTGGG CCGGGCCCTG CTCCCCTGGC 833
AGCAGAAGTG GGTGCAGGAA GGTGGCAGTG ACCAGCGCCC TGGACCATGC AGTTCGGCGG 893
10 CCGCTCTAAA GGATCCAAGC TTACGTACGC GTGCATGCGA CGTCATAGCT CTTCTATAGT 953
GTCACCTAAA TTCAATTCAC TGGCCGTCGT TTTACAACGT CCTGACTGGG AAA 1006

15 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 amino acids

(B) TYPE: amino acid

20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

25 Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu
1 5 10 15
30 Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro
20 25 30
Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg
35 35 40 45
Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu
50 55 60
40 Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His
65 70 75 80
Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro
85 90 95
45 Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys
100 105 110
Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys
115 120 125
50 Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro
130 135 140
Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala
145 150 155 160
55 Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys
165 170 175

Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu
 180 185 190

Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Leu Glu Val
 195 200 205

Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu
 210 215 220

Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp
 225 230 235 240

Val

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 723 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGCNCARC	AYGGNGCNAT	GGGNGCNTTY	MGNGCNYTNT	GYGGNYTNGC	NYTNYTNTGY	60
GCNYTNWSNY	TNGGNCARMG	NCCNACNGGN	GGNCCNGGNT	GYGGNCCNGG	NMGNYTNYTN	120
YTNGGNACNG	GNACNGAYGC	NMGNTGYTGY	MGNGTNCAYA	CNACNMGNTG	YTGymNGAY	180
TAYCCNGGNG	ARGARTGYTG	YWSNGARTGG	GAYTGYATGT	GYGTNCARCC	NGARTTYCAY	240
TGYGGNGAYC	CNTGYTGYAC	NACNTGYMGN	CAYCAYCCNT	GYCCNCCNGG	NCARGGNGTN	300
CARWSNCARG	GNAARTTYWS	NTTYGGNTTY	CARTGYATHG	AYTGYGCNWS	NGGNACNTTY	360
WSNGGNGGNC	AYGARGGNCA	YTGYAARCCN	TGGACNGAYT	GYACNCARTT	YGGNTTYTYN	420
ACNGTNTTYC	CNGGNAAYAA	RACNCAYAAY	GCNGTNTGYG	TNCCNGGNWS	NCCNCCNGCN	480
GARCCNYTNG	GNTGGYTNAc	NGTNGTNYTN	YTNGCNGTNG	CNGCNTGYGT	NYTNYTNYTN	540
ACNWSNGCNC	ARYTNGGNYT	NcAYATHTGG	CARYTNMGNW	SNCARTGYAT	GTGGCCNMGN	600
GARACNCARY	TNYTNYTNGA	RGTNCCNCCN	WSNACNGARG	AYGCNMGNWS	NTGYCARTTY	660
CCNGARGARG	ARMGNGGNGA	RMGNWSNGCN	GARGARAARG	GNMGNYTNGG	NGAYYTNTGG	720
GTN						723

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Gly	Ala	Phe	Arg	Ala	Leu	Cys	Gly	Leu	Ala	Leu	Leu	Cys	Ala	Leu	1	5	10	15
Ser	Leu	Gly	Gln	Arg	Pro	Thr	Gly	Gly	Pro	Gly	Cys	Gly	Pro	Gly	Arg	20	25	30	
Leu	Leu	Leu	Gly	Thr	Gly	Thr	Asp	Ala	Arg	Cys	Cys	Arg	Val	His	Thr	35	40	45	
Thr	Arg	Cys	Cys	Arg	Asp	Tyr	Pro	Gly	Glu	Glu	Cys	Cys	Ser	Glu	Trp	50	55	60	
Asp	Cys	Met	Cys	Val	Gln	Pro	Glu	Phe	His	Cys	Gly	Asp	Pro	Cys	Cys	65	70	75	80
Thr	Thr	Cys	Arg	His	His	Pro	Cys	Pro	Pro	Gly	Gln	Gly	Val	Gln	Ser	85	90	95	
Gln	Gly	Lys	Phe	Ser	Phe	Gly	Phe	Gln	Cys	Ile	Asp	Cys	Ala	Ser	Gly	100	105	110	
Thr	Phe	Ser	Gly	Gly	His	Glu	Gly	His	Cys	Lys	Pro	Trp	Thr	Asp	Cys	115	120	125	
Thr	Gln	Phe	Gly	Phe	Leu	Thr	Val	Phe	Pro	Gly	Asn	Lys	Thr	His	Asn	130	135	140	
Ala	Val	Cys	Val	Pro	Gly	Ser	Pro	Pro	Ala	Glu	Pro	Leu	Gly	Trp	Leu	145	150	155	160
Thr	Val	Val	Leu	Leu	Ala	Val	Ala	Ala	Cys	Val	Leu	Leu	Leu	Thr	Ser	165	170	175	
Ala	Gln	Leu	Gly	Leu	His	Ile	Trp	Gln	Leu	Arg	Lys	Thr	Gln	Leu	Leu	180	185	190	
Leu	Glu	Val	Pro	Pro	Ser	Thr	Glu	Asp	Ala	Arg	Ser	Cys	Gln	Phe	Pro	195	200	205	
Glu	Glu	Glu	Arg	Gly	Glu	Arg	Ser	Ala	Glu	Glu	Lys	Gly	Arg	Leu	Gly	210	215	220	
Asp	Leu	Trp	Val													225			

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

5 Met Gly Ala Phe Arg Ala Leu Cys Gly Leu Ala Leu Leu Cys Ala Leu
1 5 10 15

10 Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro Gly Cys Gly Pro Gly Arg
20 25 30

Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg Cys Cys Arg Val His Thr
35 40 45

15 Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu Glu Cys Cys Ser Glu Trp
50 55 60

20 Asp Cys Met Cys Val Gln Pro Glu Phe His Cys Gly Asp Pro Cys Cys
65 70 75 80

Thr Thr Cys Arg His His Pro Cys Pro Pro Gly Gln Gly Val Gln Ser
85 90 95

25 Gln Gly Lys Ser Trp Arg Cys Leu Trp Glu Ser Thr Gln Ala Arg Gly
100 105 110

Ser Thr Arg Ala Arg Gly Arg Ala Arg Gly His Arg Cys Pro Ala Arg
115 120 125

30 Thr Cys Gly Val Trp Gly Pro Glu Ser Cys Glu Ala Gly Gln Ala Arg
130 135 140

35 Pro Cys Ser Gly Thr Thr Gly His Glu Ala Leu Gly Val Ser Cys Pro
145 150 155 160

Cys Phe Leu Ser Leu Gly Phe Ser Ile Gln His Glu Gly Cys Glu Asn
165 170 175

40 Pro Ala Gly Arg Trp Gly Arg Val Pro Gly Ala Val Trp Leu Ser Gly
180 185 190

Pro Gly His Pro Ser Cys Leu Ser Ser Pro His Thr Glu Arg Ala Cys
195 200 205

45 Pro Val Pro Pro Gly Val Leu Ser Gly Ala Trp Gly Cys Thr Leu Phe
210 215 220

50 Trp Lys Glu Gln Leu Lys Ser Ser
225 230

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 311 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

10

Met Gly Ala Phe Arg Ala Leu Cys Gly Leu Ala Leu Leu Cys Ala Leu
1 5 10 15

Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro Gly Cys Gly Pro Gly Arg
20 25 30

15

Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg Cys Cys Arg Val His Thr
35 40 45

Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu Glu Cys Cys Ser Glu Trp
50 55 60

20

Asp Cys Met Cys Val Gln Pro Glu Phe His Cys Gly Asp Pro Cys Cys
65 70 75 80

25

Thr Thr Cys Arg His His Pro Cys Pro Pro Gly Gln Gly Val Gln Ser
85 90 95

Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys Ile Asp Cys Ala Ser Gly
100 105 110

30

Thr Phe Ser Gly Gly His Glu Gly His Cys Lys Pro Trp Thr Asp Cys
115 120 125

Thr Gln Phe Gly Phe Leu Thr Val Phe Pro Gly Asn Lys Thr His Asn
130 135 140

35

Ala Val Cys Val Pro Gly Ser Pro Pro Ala Glu Pro Leu Gly Trp Leu
145 150 155 160

40

Thr Val Val Leu Leu Ala Val Ala Ala Cys Val Leu Leu Leu Thr Ser
165 170 175

Ala Gln Leu Gly Leu His Ile Trp Gln Leu Arg Ser Gln Cys Met Trp
180 185 190

45

Pro Arg Gly Leu Ser Gln Pro Gly Ala Gly Arg Trp Glu His Gly Cys
195 200 205

Leu Leu Thr Val Ala Pro Leu Gln Arg Pro Ser Cys Cys Trp Arg Cys
210 215 220

50

Arg Arg Arg Pro Lys Thr Pro Glu Ala Ala Ser Ser Pro Arg Lys Ser
225 230 235 240

55

Gly Ala Ser Asp Arg Gln Arg Arg Arg Gly Gly Trp Glu Thr Cys Gly
245 250 255

Cys Glu Pro Gly Arg Pro Pro Gly Pro Pro Thr Ala Ala Ser Pro Ser
260 265 270

Pro Gly Ala Pro Gln Ala Ala Gly Ala Leu Arg Ser Ala Leu Gly Arg
275 280 285

5 Ala Leu Leu Pro Trp Gln Gln Lys Trp Val Gln Glu Gly Gly Ser Asp
290 295 300

Gln Arg Pro Gly Pro Cys Ser
305 310

10

Pro Gly Ala Pro Gln Ala Ala Gly Ala Leu Arg Ser Ala Leu Gly Arg
275 280 285
Ala Leu Leu Pro Trp Gln Gln Lys Trp Val Gln Glu Gly Gly Ser Asp
290 295 300
Gln Arg Pro Gly Pro Cys Ser
305 310